

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 16, 2005, 21:10:15 ; Search time 147.538 Seconds
(Without alignment) 1436.539 Million cell updates/sec

Title: US-10-017-168-20
Perfect score: 2795
Sequence: 1 MFRSDMPKNTAIVEISNL.....AVLENFQRFGFKDAFLKKAR 548

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04: *
1: geneseqP19908: *
2: geneseqP19908: *
3: geneseqP20018: *
4: geneseqP20018: *
5: geneseqP20018: *
6: geneseqP20018: *
7: geneseqP20018: *
8: geneseqP20048: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2178	77.9	432	AAB43316
2	1479	52.9	312	AAB43318
3	1043	37.3	232	AAB43317
4	280	10.0	2768	AAB63397
5	271	9.7	783	2 AAB05804
6	269	9.6	567	4 AAB13147
7	268.5	9.6	1000	6 AAB23647
8	259	9.3	522	4 AAE03397
9	257	9.2	412	2 AHW03626
10	250	8.9	902	4 AAB29778
11	250	8.9	1018	2 AAR91747
12	250	8.9	1018	2 AHW97039
13	250	8.9	1018	4 AAG66528
14	250	8.7	1018	8 ADU93471
15	248	8.7	360	2 AHW03627
16	242	8.7	34350	8 ADQ89364
17	236.5	8.5	2109	8 ADN23633
18	232.5	8.3	552	7 ADNC13182
19	228	8.2	1388	6 ADJ38696
20	226	8.1	553	7 ADM05820
21	224	8.0	1388	7 ADJ6333
22	223	8.0	489	4 ABBS8655
23	223	8.0	845	6 ABM04814
24	222	7.9	864	4 AAM3026
25	220.5	7.9	486	5 AAB23036

ALIGNMENTS

26	217	7.8	611	2 AAI29039	AAV29039 T. gondii
27	217	7.8	611	4 AAU5510	Aau25510 T. gondii
28	217	7.8	611	7 ADG1731	Adg1731 T. gondii
29	217	7.8	679	4 ABB59691	Abb59691 Drosophil
30	216	7.7	1501	5 AAU76762	Aau76762 Plasmodium
31	216	7.7	1568	8 ADP0152	Adp0152 Amino acid
32	213.5	7.6	382	4 AAE02399	Aae02399 Canine re
33	213	7.6	4412	3 AAY23666	Aay23666 Sequence
34	211	7.5	3551	8 ADQ01006	Adq01006 Mouse hom
35	210	7.5	1192	4 ABB59642	Abb59642 Drosophil
36	210	7.5	1965	8 ADK7314	Adk7314 Streptococ
37	210	7.5	1972	8 ADP4616	Adp4616 Novel S.
38	208.5	7.5	293	4 AAB02398	Aab02398 Canine re
39	206.5	7.4	474	8 ADN04475	Adn04475 Thermococ
40	205	7.4	869	7 ADI60170	Adi60170 Secreted
41	205	7.3	385	6 ABU20070	Abu20070 Protein e
42	204	7.3	1026	4 AAM8825	Aam8825 Human pro
43	203	7.3	1245	6 ABP56885	Abp56885 Staphyloc
44	203	7.3	2397	6 ABU43308	Abu43308 Protein e
45	201	7.2	897	4 AAU37176	Aau37176 Staphyloc

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Gencore version 5.1.6

Om protein - protein search, using sw model

Run on:

March 16, 2005, 21:10:15 ; Search time 84 Seconds

(without alignments)

1436.539 Million cell updates/sec

Title: US-10-017-168-6

Perfect score: 1572

Sequence: 1 MFTVRSDFMFPKNTAVELNSLVE.....HTKOPSHSHSVNSNAPQFRKP 312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16sec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003s:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	1572	100.0	312	4	AAB48118	Aab0318 T. pallid
2	1480	94.1	432	4	AAB48116	Aab0316 T. pallid
3	1118	71.1	232	4	AAB48317	Aab0317 T. pallid
4	214.5	13.6	1018	2	AAR9747	Aar9747 P. vivax
5	214.5	13.6	1018	2	AAR9739	Aar9739 A. secreta
6	214.5	13.6	1018	4	AAG66528	Aag66528 Plasmodium
7	13.5	8	ADJ95471	8	ADJ95471	Adj95471 Plasmodium
8	187.5	11.9	2109	8	ADN23693	Adn23693 Bacteriophage
9	187.5	11.9	2768	4	ABB61397	Abb61397 Drosophila
10	183	11.6	783	2	ADP5804	Adp5804 C-terminal
11	179	11.4	552	7	ADC31182	Adc31182 Human novel
12	171	10.9	194	4	ABG11265	Abg11265 Novel human
13	167.5	10.7	1000	5	ABJ2647	Abj2647 Aspergillus
14	159	10.1	258	2	AAW5107	Aaw5107 Streptococcus
15	159	10.1	258	5	ABP54601	Abp54601 S. pneumoniae
16	159	10.1	258	7	ADC45171	Adc45171 S. pneumoniae
17	159	10.1	553	7	ADM05820	Adm05820 Human protein
18	159	10.1	565	2	AAW61247	Aaw61247 Streptococcus
19	159	10.1	565	5	ABP54665	Abp54665 S. pneumoniae
20	159	10.1	565	7	ADC45299	Adc45299 S. pneumoniae
21	159	10.1	1881	3	AYA4506	Aya4506 Streptococcus
22	159	10.1	1881	6	ABU01047	Abu01047 S. pneumoniae
23	159	10.1	1881	8	ADM2119	Adm2119 S. pneumoniae
24	157.5	591	5	ABB2325	Abb2325 Herbicide	
25	156.5	10.0	592	4	AAB02397	Aab02397 Canine re

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16sec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003s:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16sec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003s:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16sec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003s:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

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Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16sec04:*

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4: geneseqp2001s:*

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7: geneseqp2003bs:*

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Maximum Match 100%

Listing first 45 summaries

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4: geneseqp2001s:*

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Maximum Match 100%

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4: geneseqp2001s:*

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Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16sec04:*

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4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003s:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16sec04:*

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4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003s:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16sec04:*

1: geneseqp1980s:*

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4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003s:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16sec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003s:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16sec04:*

1: geneseqp1980s:*

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3: geneseqp2000s:*

4: geneseqp2001s:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16sec04:*

1: geneseqp1980s:*

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16sec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003s:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16sec04:*

1: geneseqp1980s:*

GenCore version 5.1.6
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Om protein - protein search, using sw model

Run on: March 16, 2005, 21:14:51 ; Search time 17.7143 Seconds
 (Without alignment) 1694.657 Million cell updates/sec

Title: US-10-017-168-6
 Perfect score: 1572
 Sequence: 1 MFVRSDDMPKNTAVIEISNLRL... HTKQPSHSVSNSAPNQFRKP 312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : PIR_79;*
 1: pir1;*
 2: pir2;*
 3: pir3;*
 4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

Score Query Match Length DB ID

Description

Result No.	Score	Query Match	Length	DB ID	Description
1	963	61.3	256	2	PIR1326
2	430.5	27.4	227	2	GI1326
3	198	12.6	721	2	SG9795
4	195	12.4	407	1	BBB03
5	187.5	11.9	2109	2	BB9066
6	187.5	11.9	2109	2	TR3247
7	187	11.9	630	2	S29796
8	185	11.8	1271	2	AM5555
9	176	11.2	913	2	TR2485
10	175	11.1	391	2	S27850
11	174	11.1	450	2	C39413
12	166.5	10.6	1094	2	S49313
13	165.5	10.5	590	2	A40437
14	162	10.3	1110	2	151116
15	159	10.1	1881	2	H95076
16	157	10.0	1621	2	A82255
17	156.5	10.0	296	2	A54527
18	153.5	9.8	849	2	S00030
19	153	9.7	518	2	GG4488
20	151.5	9.6	1020	1	QPHUH
21	151	9.6	845	2	A5669
22	150	9.6	798	2	TR3022
23	150.5	9.5	679	2	S03366
24	150	9.4	1963	2	B88002
25	145.5	9.3	506	2	TR4349
26	145.5	9.3	5170	2	TR5348
27	145	9.2	644	2	S55395
28	145	9.2	837	2	TR2761

ALIGNMENTS

RESULT 1

Query Match 61.3%; Score 963; DB 2; Length 256;

Best Local Similarity 98.5%; Pred. No. 9.1e-51; Mismatches 0; Indels 0; Gaps 0;

Matches 192; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MFVRSDDMPKNTAVIEISNLRL... HTKQPSHSVSNSAPNQFRKP 312

Db 57 MFVRSDDMPKNTAVIEISNLRL... HTKQPSHSVSNSAPNQFRKP 312

Qy 61 RVRTGTTGSGSQTQDGLSLASLPSRVPARPQDPPSSPPAGHTVBYRDTVFDPR 120

Db 17 RVRTGTTGSGSQTQDGLSLASLPSRVPARPQDPLSSPPAGHTVBYRDTVFDPR 176

Qy 121 LVSPLSRVEEDVPKVVEPASEREGGEREVEDVPKVVEPASEREGGEREVEDVPKVVEPAS 180

Db 177 LVSPLSRVEEDVPKVVEPASEREGGEREVEDVPKVVEPASEREGGEREVEDVPKVVEPAS 236

Qy 181 BREGEREVEDVPKV 195

Db 237 BREGEREVEDVPKV 251

RESULT 2

hypothetical protein TF0434 - syphilis spirochete

C;Species: *Treponema pallidum* subsp. *pallidum* (syphilis spirochete)

C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C;Accession: G71326

R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwaltney, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McClory, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

GenCore version 5.1.6																		
Copyright (c) 1993 - 2005 Compugen Ltd.																		
OM protein - protein search, using SW model																		
Run on:	March 16, 2005, 21:13:20 ; Search time 79.1429 Seconds																	
Title:	US-10-017-168-6																	
Perfect score:	1572																	
Sequence:	1 MFVRSDMPKNTAELVSNLE.....HTKQPSSHSVNSNAPNQFRKP 312																	
Scoring table: BLASTSUM2																		
Searched:	Gapext 0.5																	
Total number of hits satisfying chosen parameters:	1612378																	
Minimum DB seq length: 0																		
Maximum DB seq length: 200000000																		
Post-processing: Minimum Match 0% ; Maximum Match 100% ; Listing first 45 summaries																		
Database :	UniProt_03;* 1: uniprot_sprot;* 2: uniprot_trembl;*																	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.																		
SUMMARIES																		
Result No.	Score	Query Match	Length	DB ID	Description	RESULT	1	ALIGNMENTS										
1	1567	99.7	428	2	Q9ALV6	Q9ALV6	PRELIMINARY;	PRT;	428 AA.									
2	1480	94.1	432	2	Q91953	Q9ALV6;	AC	DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)									
3	1479	94.1	548	2	Q93CA4	Q9ALV6;	DT	DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)									
4	1365.5	86.8	393	2	Q93CA3	Q91953	Best Local Similarity 99.7%; Pred. No. 8. 3e-79;	DE	01-OCT-2002 (TREMBLrel. 22, Last annotation update)									
5	1113	70.8	248	2	Q9ALV7	Q9ALV7	Matches 311; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	GN	Acidic repeat protein.									
6	963	61.3	256	2	Q83448	Q91953	Name=arp, pallidum subsp. endemicum.	OS	Treponema pallidum subsp. endemicum, Spirochaetales, Spirochaetaceae, Treponemataceae.									
7	430.5	27.4	227	2	Q83449	Q83448	Treponema p	OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponemataceae.									
8	345.5	22.0	227	2	Q83449	Q83449	Treponema p	OX	NCBI_TaxID:53435;									
9	242.5	15.6	432	2	Q964C9	Q964C9	Treponema p	RP	[1]									
10	237.5	15.1	1112	2	Q63G96	Q964C9	Treponema p	RC	SEQUENCE FROM N.A.									
11	220.8	14.5	410	2	Q962I4	Q962I4	Treponema p	RL	SEQUENCE FROM N.A.									
12	215	13.7	1167	2	Q7SH94	Q7SH94	Treponema p	RA	STRAIN=Bohemia;									
13	211	13.4	466	2	Q6NE60	Q7SH94	Treponema p	RA	Liu H., Steiner B.M., Rodes B.; Submitted (SEP-001) to the EMBL/GenBank/DBJ databases.									
14	208.5	13.3	1070	2	Q81Y70	Q81Y70	Treponema p	RA	Liu H., Steiner B.M., Rodes B.; Submitted (SEP-001) to the EMBL/GenBank/DBJ databases.									
15	206	13.1	5458	2	Q9U459	Q81Y70	Treponema p	RA	STRAIN=Bosnia;									
16	202.5	12.9	394	2	Q964D0	Q964D0	Treponema p	RA	STRAIN=Bosnia;									
17	202.5	12.9	453	1	PTP1_ENCHE	Q964D0	Treponema p	RA	STRAIN=Bosnia;									
18	198.5	12.6	248	2	Q9LRH2	Q9LRH2	Treponema p	RA	STRAIN=Bosnia;									
19	198	12.6	721	1	YCF2_OENPI	Q9LRH2	Treponema p	RA	STRAIN=Bosnia;									
20	195	12.4	407	1	IE68_SHV21	YCF2_OENPI	Treponema p	RA	STRAIN=Bosnia;									
21	190.5	12.1	614	2	Q94674	IE68_SHV21	Treponema p	RA	STRAIN=Bosnia;									
22	189.5	12.1	690	2	Q96PC5	Q94674	Treponema p	RA	STRAIN=Bosnia;									
23	187.5	11.9	2768	2	Q99VCO	Q96PC5	Treponema p	RA	STRAIN=Bosnia;									
24	187.5	11.9	10578	2	Q98IS5	Q99VCO	Treponema p	RA	STRAIN=Bosnia;									
25	187.5	11.9	18519	2	Q81SF6	Q98IS5	Treponema p	RA	STRAIN=Bosnia;									
26	187.5	11.9	18534	2	Q81SF7	Q81SF6	Treponema p	RA	STRAIN=Bosnia;									
27	187	11.9	630	1	YCF2_OENVI	Q81SF7	Treponema p	RA	STRAIN=Bosnia;									
28	186	11.8	982	2	Q6CG75	YCF2_OENVI	Treponema p	RA	STRAIN=Bosnia;									
29	185	11.8	1271	2	Q25860	Q6CG75	Treponema p	RA	STRAIN=Bosnia;									
30	182	11.6	1108	2	Q9ND10	Q25860	Treponema p	RA	STRAIN=Bosnia;									
31	181.5	11.5	1554	2	Q7RMX1	Q9ND10	Treponema p	RA	STRAIN=Bosnia;									

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OM protein - protein search, using Bw model

Run on: March 16, 2005, 21:10:15 ; Search time 62.4615 Seconds

(without alignments) 1436.539 Million cell updates/sec

Title: US-10-017-168-4
Perfect score: 1168

Sequence: 1 MFRSDMPKNTAVIENL... HTKOPSHSVNSNSAPNQFRKP 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

1	1168	100.0	232	4	AB48317	ab48317 T. pallid
2	1118	95.7	312	4	AB48318	ab48318 T. pallid
3	1048	89.7	432	4	AB48316	ab48316 T. pallid
4	138.5	11.9	1018	2	AB498747	ab498747 P. vivax
5	138.5	11.9	1018	2	AB497039	ab497039 A secrete
6	138.5	11.9	1018	4	AB466528	ab466528 Plasmodiu
7	138.5	11.9	1018	8	AB495471	ab495471 Plasmodiu
8	137	11.7	25	4	AB48324	ab48324 T. pallid
9	124.5	10.7	2109	8	AB423693	ab423693 Bacterial
10	124.5	10.7	19938	6	AB276681	ab276681 Streptomy
11	124	10.6	25	4	AB48323	ab48323 T. pallid
12	122	10.4	676	4	AB411370	ab411370 Novel hum
13	122	10.4	676	4	AB429412	ab429412 Novel hum
14	122	10.4	676	4	AB411395	ab411395 Novel hum
15	121	10.4	26	4	AB48326	ab48326 T. pallid
16	121	10.4	2768	4	AB468397	ab468397 Drosophil
17	119.5	10.2	1991	6	AB052986	ab052986 Human put
18	119.5	10.2	2263	7	AD770425	ad770425 Human hea
19	119.5	10.2	2296	8	AD60280	ad60280 Human spl
20	119.5	10.2	2152	8	AD60278	ad60278 Human ser
21	119.5	10.2	2752	8	AD60278	ad60278 Human ser
22	117.5	10.1	540	6	ABr44276	ab44276 Novel hum
23	117	10.0	278	2	ABW55109	abw55109 Streptoco
24	117	10.0	278	5	ABp54603	abp54603 S. pneumo
25	117	10.0	278	7	ADC45175	adc45175 S. pneumo

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. Score Query Match Length DB ID Description

1	116	10.0	258	7	ADC45171	adc45171 S. pneumo
2	116	9.9	552	7	ADC31182	adc31182 Human nov
3	116	9.9	565	2	RAW61247	raw61247 Streptoco
4	116	9.9	565	4	ABP56665	abp56665 S. pneumo
5	116	9.9	565	7	ADC45299	adc45299 S. pneumo
6	116	9.9	1881	3	AYA4506	aya4506 Streptoco
7	116	9.9	1881	6	ABU0147	abu0147 S. pneumo
8	116	9.9	1881	8	ADM92119	adm92119 S. pneumo
9	113	9.7	456	4	ABB58301	abb58301 Drosophil

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. Score Query Match Length DB ID Description

1	117	10.0	571	2	ABP54558	abp54558 S. pneumo
2	117	10.0	571	7	ADC45085	adc45085 S. pneumo
3	117	10.0	1963	6	ABU46054	abu46054 protein e
4	117	10.0	1965	2	AAW69165	aww69165 Streptoco
5	117	10.0	1965	8	ADK47114	adk47114 Streptoco
6	117	10.0	1972	8	ADR9416	adr9416 Novel S.
7	117	10.0	2004	6	ABU1577	abu1577 S. pneumo
8	117	10.0	2004	8	ADM92167	adm92167 S. pneumo
9	117	10.0	2004	8	AWW61247	aww61247 Streptoco
10	117	10.0	2004	8	ABP56665	abp56665 S. pneumo
11	117	10.0	2004	8	ADC45299	adc45299 S. pneumo
12	117	10.0	2004	8	ADM92119	adm92119 S. pneumo
13	117	10.0	2004	8	ABB58301	abb58301 Drosophil

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. Score Query Match Length DB ID Description

1	117	10.0	571	2	AAW55064	aww55064 Streptoco
2	117	10.0	571	7	ABP54558	abp54558 S. pneumo
3	117	10.0	571	7	ADC45085	adc45085 S. pneumo
4	117	10.0	1963	6	ABU46054	abu46054 protein e
5	117	10.0	1965	2	AAW69165	aww69165 Streptoco
6	117	10.0	1965	8	ADK47114	adk47114 Streptoco
7	117	10.0	1972	8	ADR9416	adr9416 Novel S.
8	117	10.0	2004	6	ABU1577	abu1577 S. pneumo
9	117	10.0	2004	8	ADM92167	adm92167 S. pneumo
10	117	10.0	2004	8	AWW61247	aww61247 Streptoco
11	117	10.0	2004	8	ABP56665	abp56665 S. pneumo
12	117	10.0	2004	8	ADC45299	adc45299 S. pneumo
13	117	10.0	2004	8	ADM92119	adm92119 S. pneumo
14	117	10.0	2004	8	ABB58301	abb58301 Drosophil

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. Score Query Match Length DB ID Description

1	117	10.0	571	5	ABP54558	abp54558 S. pneumo
2	117	10.0	571	7	ADC45085	adc45085 S. pneumo
3	117	10.0	1963	6	ABU46054	abu46054 protein e
4	117	10.0	1965	2	AAW69165	aww69165 Streptoco
5	117	10.0	1965	8	ADK47114	adk47114 Streptoco
6	117	10.0	1972	8	ADR9416	adr9416 Novel S.
7	117	10.0	2004	6	ABU1577	abu1577 S. pneumo
8	117	10.0	2004	8	ADM92167	adm92167 S. pneumo
9	117	10.0	2004	8	AWW61247	aww61247 Streptoco
10	117	10.0	2004	8	ABP56665	abp56665 S. pneumo
11	117	10.0	2004	8	ADC45299	adc45299 S. pneumo
12	117	10.0	2004	8	ADM92119	adm92119 S. pneumo
13	117	10.0	2004	8	ABB58301	abb58301 Drosophil

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. Score Query Match Length DB ID Description

1	117	10.0	571	5	ABP54558	abp54558 S. pneumo
2	117	10.0	571	7	ADC45085	adc45085 S. pneumo
3	117	10.0	1963	6	ABU46054	abu46054 protein e
4	117	10.0	1965	2	AAW69165	aww69165 Streptoco
5	117	10.0	1965	8	ADK47114	adk47114 Streptoco
6	117	10.0	1972	8	ADR9416	adr9416 Novel S.
7	117	10.0	2004	6	ABU1577	abu1577 S. pneumo
8	117	10.0	2004	8	ADM92167	adm92167 S. pneumo
9	117	10.0	2004	8	AWW61247	aww61247 Streptoco
10	117	10.0	2004	8	ABP56665	abp56665 S. pneumo
11	117	10.0	2004	8	ADC45299	adc45299 S. pneumo
12	117	10.0	2004	8	ADM92119	adm92119 S. pneumo
13	117	10.0	2004	8</		

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(c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 16, 2005, 21:13:20 ; Search time 58.8498 Seconds
(without alignments)

Sequence: US-10-017-168-4
1 MFVRSDMFPKNTAVEISNL... HTKOPSHSVNSAPNQFRKP 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:

1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1163	99.6	348	2 Q9ALV7	Q9ALV7 treponema p
2	1130.5	96.8	393	2 Q93CA3	Q93CA3 treponema p
3	1113	95.3	428	2 Q9ALV6	Q9ALV6 treponema p
4	1048	89.7	432	2 Q91953	Q91953 treponema p
5	1043	89.3	548	2 Q93CA4	Q93CA4 treponema p
6	963	82.4	256	2 Q93448	Q93448 treponema p
7	429	36.7	227	2 Q93449	Q93449 treponema p
8	286	24.5	458	2 Q93NG7	Q93NG7 treponema p
9	162	13.9	410	2 Q96214	Q96214 treponema p
10	160	13.7	432	2 Q964C0	Q964C0 treponema p
11	152.5	13.1	466	2 Q96NE60	Q96NE60 treponema p
12	147	12.6	394	2 Q964AD	Q964AD treponema p
13	147	12.6	453	1 P7P1 ENCH	P7P1 ENCH
14	146.5	12.5	167	2 Q7SH94	Q7SH94 treponema p
15	144.5	12.4	1070	2 Q81YTO	Q81YTO treponema p
16	144	12.3	1112	2 Q63G95	Q63G95 treponema p
17	133.5	11.4	891	2 Q66NVT0	Q66NVT0 treponema p
18	129	11.0	675	2 Q871R0	Q871R0 treponema p
19	126.5	10.8	614	2 Q94674	Q94674 treponema p
20	125.5	10.7	519	2 Q7S118	Q7S118 treponema p
21	125.5	10.7	915	2 Q6FPM18	Q6FPM18 treponema p
22	125	10.7	10578	2 Q81SP5	Q81SP5 treponema p
23	124.5	10.7	18519	2 Q81SF6	Q81SF6 treponema p
24	124.5	10.7	18534	2 Q81SF7	Q81SF7 treponema p
25	123.5	10.6	796	2 Q96579	Q96579 treponema p
26	122	10.4	1942	2 Q7NAY2	Q7NAY2 treponema p
27	121.5	10.4	690	2 Q6PC52	Q6PC52 treponema p
28	121	10.4	687	2 Q7S73	Q7S73 treponema p
29	121	10.4	2768	2 Q9VC00	Q9VC00 treponema p
30	120	10.3	1754	2 Q80U37	Q80U37 treponema p
31	120	10.3	2607	2 Q8BT18	Q8BT18 treponema p

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	393 AA.
ID	Q9ALV7			
AC	Q9ALV7;			
DT	01-JUN-2001 (TREMBrel. 17, Created)			
DT	01-DEC-2001 (TREMBrel. 19, Last sequence update)			
DR	01-OCT-2002 (TREMBrel. 22, Last annotation update)			
GN	Name-arp;			
OS	Treponema pallidum (subsp. pertenue) (Yaws treponeme), Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.			
OC	OX NCBI_TAXID=168;			
RN	[1]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA STRAIN=CDC2;			
RL	RL Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[7]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[8]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[9]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[10]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[11]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[12]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[13]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[14]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[15]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[16]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[17]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[18]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[19]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[20]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[21]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[22]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[23]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[24]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[25]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[26]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[27]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[28]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[29]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[30]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[31]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[32]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[33]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[34]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[35]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[36]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[37]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[38]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[39]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[40]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[41]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[42]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[43]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[44]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
RN	[45]			
RR	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	RA Liu H., Steiner B.M., Rodes B.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			

Q93CA3 PRELIMINARY; PRT; 393 AA.

Q93CA3; Q93CA3; PRELIMINARY; PRT; 393 AA.</

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OM protein - protein search, using bw model

Run on: March 16, 2005, 21:14:51 ; Search time 13.1722 Seconds
(Without alignments)
1694.657 Million cell updates/sec

Title: US_10-017-168-4
Perfect score: 1168

Sequence: 1 MFVRSDMPKNTAVELSNLRL...HTKQPSHISVNSNAPQRK 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79,*
1: pir1,*
2: pir2,*
3: pir3,*
4: pir4,*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score % Query Match length DB ID Description

1 963 82.4 256 2 P71326 hypothetical protein TR0433 - syphilis spirochete
2 429 36.7 227 2 G71326 hypothetical prote
3 124.5 10.7 2109 2 S89066 protein H0509_1
4 124.5 10.7 2109 2 T33247 hypothetical prote
5 119.5 10.2 1791 2 T02345 hypothetical prote
6 119 10.2 1012 2 I53172 hypothetical prote
7 118 10.1 630 2 S29796 RAB-28 - mouse
8 117.5 10.1 590 2 A40437 hypothetical prote
9 117 10.0 1621 2 A82255 glutamyl acid-rich
10 117 10.0 1963 2 B98002 hypothetical prote
11 117 10.0 2004 2 F95133 IGA specific metal
12 116 9.9 1881 2 H95076 immunoglobulin A1
13 116 9.8 407 1 EDBE03 zinc metalloprotei
14 114 9.8 450 1 C29413 immediate-early r
15 113.5 9.7 1384 2 T26656 ubiquinol-cytochrome
16 113.5 9.7 1611 2 T38235 hypothetical prote
17 113 9.7 1078 2 T42712 myelin transcripti
18 112 9.6 880 2 D89756 protein T23E7_2b [
19 111.5 9.5 798 2 T33022 hypothetical prote
20 111 9.5 391 2 S27850 surface antigen Tc
21 110.5 9.5 184 2 S48035 hypothetical prote
22 109.5 9.4 630 2 T28700 hypothetical prote
23 109 9.3 721 2 S29795 hypothetical prote
24 108.5 9.3 554 2 JW0094 hypothetical prote
25 108 9.2 585 2 T47364 hypothetical prote
26 108 9.2 304 2 S44897 ZK126.2 protein-
27 108 9.2 1566 2 A43607 cell surface antigen
28 107.5 9.2 1390 2 T14004 trfA protein - sli
29 107.5 9.2 2440 2 S39162 transcription coac

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1	963	82.4	256	2 P71326	hypothetical protein TR0433 - syphilis spirochete
2	429	36.7	227	2 G71326	hypothetical prote
3	124.5	10.7	2109	2 S89066	protein H0509_1
4	124.5	10.7	2109	2 T33247	hypothetical prote
5	119.5	10.2	1791	2 T02345	hypothetical prote
6	119	10.2	1012	2 I53172	RAB-28 - mouse
7	118	10.1	630	2 S29796	hypothetical prote
8	117.5	10.1	590	2 A40437	glutamyl acid-rich
9	117	10.0	1621	2 A82255	hypothetical prote
10	117	10.0	1963	2 B98002	IGA specific metal
11	117	10.0	2004	2 F95133	immunoglobulin A1
12	116	9.9	1881	2 H95076	zinc metalloprotei
13	116	9.8	407	1 EDBE03	immediate-early r
14	114	9.8	450	1 C29413	ubiquinol-cytochrome
15	113.5	9.7	1384	2 T26656	hypothetical prote
16	113.5	9.7	1611	2 T38235	hypothetical prote
17	113	9.7	1078	2 T42712	myelin transcripti
18	112	9.6	880	2 D89756	protein T23E7_2b [
19	111.5	9.5	798	2 T33022	hypothetical prote
20	111	9.5	391	2 S27850	surface antigen Tc
21	110.5	9.5	184	2 S48035	hypothetical prote
22	109.5	9.4	630	2 T28700	hypothetical prote
23	109	9.3	721	2 S29795	hypothetical prote
24	108.5	9.3	554	2 JW0094	hypothetical prote
25	108	9.2	585	2 T47364	hypothetical prote
26	108	9.2	304	2 S44897	ZK126.2 protein-
27	108	9.2	1566	2 A43607	cell surface antigen
28	107.5	9.2	1390	2 T14004	trfA protein - sli
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9	117	10.0	1621	2 A82255	hypothetical prote
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11	117	10.0	2004	2 F95133	immunoglobulin A1
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13	116	9.8	407	1 EDBE03	immediate-early r
14	114	9.8	450	1 C29413	ubiquinol-cytochrome
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20	111	9.5	391	2 S27850	surface antigen Tc
21	110.5	9.5	184	2 S48035	hypothetical prote
22	109.5	9.4	630	2 T28700	hypothetical prote
23	109	9.3	721	2 S29795	hypothetical prote
24	108.5	9.3	554	2 JW0094	hypothetical prote
25	108	9.2	585	2 T47364	hypothetical prote
26	108	9.2	304	2 S44897	ZK126.2 protein-
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24	108.5	9.3	554	2 JW0094	hypothetical prote
25	108	9.2	585	2 T47364	hypothetical prote
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